OM nucleic - nucleic search, using sw model

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GenCore version 4.5

Run on: March 9, 2002, 00:48:38 ; Search time 2351.15 Seconds
                (without alignments)
                175.416 Million cell updates/sec

Title: US-09-851-670-12
Perfect score: 25
Sequence: 1 acagctcgccccattaacatattc 25

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 824589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : GenEmbl:*
    1: gb_ba:*
    2: gb_htg:*
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   26: em_sts:*
   27: em_sy:*
   28: em_un:*
   29: em_vi:*
   30: em_htgo_hum:*
   31: em_htgo_inv:*
   32: em_htgo_rod:*
   33: em_htg_hum:*
   34: em_htg_inv:*
   35: em_htg_rod:*
   36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
1		14.6	58.4	58	6	A48495	A48495 Sequence 16
2		14	56.0	50	6	AX097513	AX097513 Sequence 8
3	c	13.6	54.4	40	6	A84763	A84763 Sequence 15
4		13.6	54.4	57	6	A60847	A60847 Sequence 15
5	c	13.4	53.6	20	6	AX004424	AX004424 Sequence
6	c	13.4	53.6	29	6	AX137235	AX137235 Sequence
7	c	13.4	53.6	29	6	AX137236	AX137236 Sequence
8	c	13.4	53.6	36	6	A66390	A66390 Sequence 31
9	c	13.4	53.6	50	6	AX165076	AX165076 Sequence
10	c	13.4	53.6	58	6	A60214	A60214 Sequence 10
11	c	13.2	52.8	34	6	AR122290	AR122290 Sequence
12	c	13.2	52.8	34	6	AR092439	AR092439 Sequence
13	c	13.2	52.8	60	6	A29441	A29441 sequence ex
14	c	13	52.0	36	6	A66389	A66389 Sequence 31
15	c	13	52.0	50	10	AF071603	AF071603 Mus muscu
16	c	13	52.0	51	6	AX158449	AX158449 Sequence
17	c	12.8	51.2	48	6	I04372	I04372 Sequence 7
18	c	12.8	51.2	48	6	I04381	I04381 Sequence 16
19	c	12.8	51.2	51	6	AX165555	AX165555 Sequence
20	c	12.8	51.2	51	9	HSA010893	HSA010893 Homo sapi
21	c	12.6	50.4	32	6	AR082457	AR082457 Sequence
22	c	12.6	50.4	32	6	AR139013	AR139013 Sequence
23	c	12.6	50.4	38	6	AR047603	AR047603 Sequence
24	c	12.6	50.4	38	6	I54655	I54655 Sequence 23
25	c	12.6	50.4	50	6	AX097514	AX097514 Sequence
26	c	12.6	50.4	51	6	AX163122	AX163122 Sequence
27	c	12.6	49.6	21	6	AR051089	AR051089 Sequence
28	c	12.4	49.6	25	6	AX042678	AX042678 Sequence
29	c	12.4	49.6	25	6	AX043404	AX043404 Sequence
30	c	12.4	49.6	25	6	AX117676	AX117676 Sequence
31	c	12.4	49.6	30	6	AX035615	AX035615 Sequence
32	c	12.4	49.6	34	6	I81202	I81202 Sequence 7
33	c	12.4	49.6	36	6	AR031315	AR031315 Sequence
34	c	12.4	49.6	36	6	I84454	I84454 Sequence 2
35	c	12.4	49.6	40	6	I30556	I30556 Sequence 4
36	c	12.4	49.6	51	6	AX117677	AX117677 Sequence
37		12.4	49.6	54	6	AR083889	AR083889 Sequence
38		12.4	48.8	19	6	AX130042	AX130042 Sequence
39		12.2	48.8	21	6	AR138965	AR138965 Sequence
40	c	12.2	48.8	28	6	AR011468	AR011468 Sequence
41	c	12.2	48.8	28	6	AX188479	AX188479 Sequence
42	c	12.2	48.8	28	6	I18106	I18106 Sequence 34
43		12.2	48.8	37	6	AX039155	AX039155 Sequence
44		12.2	48.8	42	6	AR049554	AR049554 Sequence
45		12.2	48.8	42	6	AR049555	AR049555 Sequence

RESULT   1
A48495

LOCUS	A48495	58 bp	DNA	PAT	07-MAR-1997

DEFINITION Sequence 16 from Patent WO9602654.
ACCESSION   A48495
VERSION   A48495.1 GI:2302273
KEYWORDS   .
SOURCE   synthetic construct.
  ORGANISM synthetic construct
            artificial sequence.
REFERENCE   1 (bases 1 to 58)
  AUTHORS   Jacobs,E., Silvestre,N., Mougin,B., Bissardon,O. and Jolivet,M.
  TITLE   CONDIT TOXOPLASMA P30 EXPRESSION CASSETTE
            TRANSGENE SA (FR)
  JOURNAL   Patent: WO 9602654-A 16 01-FEB-1996;
COMMENT   Other publication FR 2722508 960119.
FEATURES   Location/Qualifiers
     source   1..58
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"

ALIGNMENTS

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BASE COUNT      17 a     21 c     13 g      7 t
ORIGIN

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        Matches   17;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;
                                                   Pred. No. 1.3e+04;

Qy    1 acagagctcgccccattaaacat 21
        |||||| ||| ||| |||| |||
Db   25 ACAGCTAGCCACCATCACCAT 45

RESULT 2
LOCUS       AX097513/c                50 bp    DNA           PAT   30-MAR-2001
DEFINITION  Sequence 32 from Patent WO0118217.
ACCESSION   AX097513
VERSION     AX097513.1  GI:13514145
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Peredeltchouk,M., Vonstein,V. and Demirjian,D.
  TITLE     Thermus promoters for gene expression
  JOURNAL   Patent: WO 0118217-A 32 15-MAR-2001;
            Thermogen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Putative promoter sequence"
BASE COUNT      16 a     11 c      8 g     15 t
ORIGIN

        Query Match
        Best Local Similarity   56.0%;   77.3%;   Score 14;    DB 6;  Length 50;
        Matches   17;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;
                                                   Pred. No. 2.6e+04;

Qy    1 acagctcgccccattaacata 22
        ||||||||||| |||||||
Db   22 AAAGCTCGCTTCCTTTAACAAA 1

RESULT 3
LOCUS       A84763                    40 bp    DNA           PAT   21-JAN-2000
DEFINITION  Sequence 8 from Patent WO9844135.
ACCESSION   A84763
VERSION     A84763.1  GI:6733631
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Hegemann,J. and Zimmermann,F.K.
  TITLE     METHOD FOR SCREENING ANTIMYCOTICALLY ACTIVE SUBSTANCES
  JOURNAL   Patent: WO 9844135-A 8 08-OCT-1998;
            HEGEMANN JOHANNES (DE); ZIMMERMANN FRIEDRICH KARL (DE)
FEATURES             Location/Qualifiers
     source          1..40
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       9 a     13 c      7 g     11 t
ORIGIN
     exon            1..40

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        Best Local Similarity   54.4%;   80.0%;   Score 13.6;  DB 6;  Length 40;
        Matches   16;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;
                                                   Pred. No. 4e+04;
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Qy    6 tcgccccattaaacatattc 25
        || ||| || |||||||||||
Db   17 TCTACCTATGAACATATTC 36

RESULT 4
LOCUS       A60847                    57 bp    DNA           PAT   06-MAR-1998
DEFINITION  Sequence 156 from Patent WO9708320.
ACCESSION   A60847
VERSION     A60847.1  GI:3715468
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 57)
  AUTHORS   Knappik,A., Pack,P., Ilag,V., Ge,L., Moroney,S. and Plueckthun,A.
  TITLE     PROTEIN/(POLY)PEPTIDE LIBRARIES
  JOURNAL   Patent: WO 9708320-A 156 06-MAR-1997;
            MORPHOSYS PROTEINOPTIMIERUNG (DE)
FEATURES             Location/Qualifiers
     source          1..57
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      14 a     16 c     14 g     13 t
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        Query Match
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        Matches   16;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;
                                                   Pred. No. 4.1e+04;

Qy    5 ctcgccccattaacatatt 24
        ||||| | |||||| | |||
Db   17 CTCGCCACGATTAAAAGATT 36

RESULT 5
LOCUS       AX004424                  20 bp    DNA           PAT   24-AUG-2000
DEFINITION  Sequence 6 from Patent WO9916899.
ACCESSION   AX004424
VERSION     AX004424.1  GI:9927883
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Anctil,J.L. and Cote,G.
  TITLE     Molecular diagnostic of glaucomas associated with chromosomes 2 and
            6
  JOURNAL   Patent: WO 9916899-A 6 08-APR-1999;
            ANCTIL JEAN LOUIS (CA); COTE GILLES (CA)
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="OLIGONUCLEOTIDE"
BASE COUNT       7 a      6 c      2 g      5 t
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        Matches   14;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;
                                                   Pred. No. 5.1e+04;

Qy   10 cccattaacatatt 24
        |||||||||||| |||
Db    1 CCCATTAACAAATT 15

RESULT 6
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AX137235
LOCUS       AX137235           29 bp    DNA                PAT       30-MAY-2001
DEFINITION  Sequence 86 from Patent EP1092764.
ACCESSION   AX137235
VERSION     AX137235.1  GI:14273561
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 29)
AUTHORS     Bartok,A., Mueh,T. and Rueckel,M.
TITLE       Continuous fermentation process
JOURNAL     Patent: EP 1092764-A 86 18-APR-2001;
            F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1..29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT      6 a      11 c      6 g      6 t
ORIGIN

Qy          3 agctcgccccattaacatattc 25
              |||||||||||||||||||| |||
Db          7 AGCTCCCCTCGAGAACCATCTTC 29

Query Match             53.6%;  Score 13.4;  DB 6;  Length 29;
Best Local Similarity   73.9%;  Pred. No. 5.1e+04;
Matches    17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

RESULT  7
AX137236/c
LOCUS       AX137236           29 bp    DNA                PAT       30-MAY-2001
DEFINITION  Sequence 87 from Patent EP1092764.
ACCESSION   AX137236
VERSION     AX137236.1  GI:14273562
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 29)
AUTHORS     Bartok,A., Mueh,T. and Rueckel,M.
TITLE       Continuous fermentation process
JOURNAL     Patent: EP 1092764-A 87 18-APR-2001;
            F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1..29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT      6 a      6 c      11 g      6 t
ORIGIN

Qy          3 agctcgccccattaacatattc 25
              ||||||| ||| | ||||| |||
Db         23 AGCTCGCCCTCGAGAACCATCTTC 1

Query Match             53.6%;  Score 13.4;  DB 6;  Length 29;
Best Local Similarity   73.9%;  Pred. No. 5.1e+04;
Matches    17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

RESULT  8
A66390/c
LOCUS       A66390             36 bp    DNA                PAT       29-MAR-1999
DEFINITION  Sequence 317 from Patent WO9741440.
ACCESSION   A66390
VERSION     A66390.1  GI:4538077
KEYWORDS
SOURCE      unidentified.
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ORGANISM    unidentified
            unclassified.
REFERENCE   1  (bases 1 to 36)
AUTHORS     Burg,S.H., Kast,W.M., Toes,R.E., Offringa,R., Melief,C. and
            Johannes,M.
TITLE       METHODS FOR SELECTING AND PRODUCING SAID SELECTED EPITOPES AND
            VACCINES INCORPORATING T CELL PEPTIDE EPITOPES AND
JOURNAL     Patent: WO 9741440-A 317 06-NOV-1997;
            UNIV LEIDEN (NL)
FEATURES             Location/Qualifiers
     source          1..36
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT     10 a      6 c      10 g      10 t
ORIGIN

Qy          2 cagctcgccccattaacatatt 23
              ||||||||||||||||| |||
Db         34 CCGCTPAGAGCCCATTACAAPATT 12

Query Match             53.6%;  Score 13.4;  DB 6;  Length 36;
Best Local Similarity   73.9%;  Pred. No. 5.1e+04;
Matches    17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

RESULT  9
AX165076
LOCUS       AX165076           50 bp    DNA                PAT       22-JUN-2001
DEFINITION  Sequence 271 from Patent WO0138586.
ACCESSION   AX165076
VERSION     AX165076.1  GI:14545905
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
AUTHORS     Shinkets,R.A. and Leach,M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0138586-A 271 31-MAY-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25..26
                     /note="Nucleotide deleted between bases 25 and 26
     variation       26
                     /note="single nucleotide polymorphism"
                     Accession number cg4403019G"
BASE COUNT     11 a      17 c      7 g      15 t
ORIGIN

Qy          2 cagctcgccccattaacatatt 24
              |||||||||||||||||| |||
Db         17 CAGCTCACCCCCATPAAGACCATT 39

Query Match             53.6%;  Score 13.4;  DB 6;  Length 50;
Best Local Similarity   73.9%;  Pred. No. 5.1e+04;
Matches    17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

RESULT  10
A60214
LOCUS       A60214             58 bp    DNA                PAT       06-MAR-1998
DEFINITION  Sequence 10 from Patent WO9708330.
ACCESSION   A60214
VERSION     A60214.1  GI:3715222
KEYWORDS
SOURCE      unidentified.
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ORGANISM   unidentified
             unclassified.
REFERENCE   1 (bases 1 to 58)
AUTHORS   Collins,M.K., Weiss,R.A., Takeuchi,Y. and Cosset,F.
TITLE   EXPRESSION SYSTEMS
JOURNAL   Patent: WO 9708330-A 10 06-MAR-1997;
             CANCER RES CAMPAIGN TECH (GB)
FEATURES
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BASE COUNT   15 a   19 c   12 g   12 t
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Qy   2 cagctcgcccccattaacatatt 24
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Db   25 CAGCCGGCCACCATGAAAACATT 47

RESULT 11
LOCUS   AR122290   58 bp   DNA   PAT
DEFINITION   Sequence 10 from patent US 6165715.
ACCESSION   AR122290
VERSION   AR122290.1   GI:14106607
KEYWORDS
SOURCE   Unknown.
ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 58)
AUTHORS   Collins,M.Katherine Levinge, Weiss,R.Anthony, Takeuchi,Y. and
             Cosset,F.
TITLE   Expression systems
JOURNAL   Patent: US 6165715-A 10 26-DEC-2000;
FEATURES
  source   1..58
             /organism="unknown"
ORIGIN

Query Match   53.6%; Score 13.4; DB 6; Length 58;
Best Local Similarity 73.9%; Pred. No. 5.1e+04;
Matches   17; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   2 cagctcgcccccattaacatatt 24
         |||| ||| ||||| ||||| |||
Db   25 CAGCCGGCCACCATGAAAACATT 47

RESULT 12
LOCUS   AR092439   34 bp   DNA   PAT
DEFINITION   Sequence 21 from patent US 5998164.
ACCESSION   AR092439
VERSION   AR092439.1   GI:10019193
KEYWORDS
SOURCE   Unknown.
ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 34)
AUTHORS   Li,Y., Cao,L., Ni,J., Gentz,R., Bult,C.J., Sutton,G.G. III and
             Rosen,C.A.
TITLE   Polynucleotides encoding human G-protein coupled receptor GPR2
JOURNAL   Patent: US 5998164-A 21 07-DEC-1999;
FEATURES
  source   1..34
             /organism="unknown"

                                                                    08-SEP-2000

BASE COUNT   11 a   11 c   6 g   6 t
ORIGIN

Query Match   52.8%; Score 13.2; DB 6; Length 34;
Best Local Similarity 83.3%; Pred. No. 6.4e+04;
Matches   15; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   3 agctcgcccccattaaca 20
         ||| ||| |||| ||| ||||
Db   6 AGCTTGCCACCATGAACA 23

RESULT 13
LOCUS   A29441   60 bp   DNA   PAT
DEFINITION   Sequence expressed in pre-B cells.
ACCESSION   A29441
VERSION   A29441.1   GI:1831980
KEYWORDS
SOURCE   synthetic construct.
ORGANISM   synthetic construct
             artificial sequence.
REFERENCE   1 (bases 1 to 60)
AUTHORS   Bauer,S.R., Kudo,A., Melchers,G.F. and Sakaguchi,N.
TITLE   Nucleotide sequences which are selectively expressed in pre-B cells
             and probes therefor.
JOURNAL   Patent: EP 0269127-A 59 01-JUN-1988;
             F. HOFFMANN-LA ROCHE AG
FEATURES
  source   1..60
             /organism="synthetic construct"
             /db_xref="taxon:32630"

                                                                    22-AUG-1996

BASE COUNT   10 a   21 c   13 g   16 t
ORIGIN

Query Match   52.8%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 6.4e+04;
Matches   15; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   8 gccccccattaacatattc 25
         ||| |||||| ||| ||||||
Db   34 GCCACCATTAGCATCTTC 51

RESULT 14
LOCUS   A66389   36 bp   DNA   PAT
DEFINITION   Sequence 316 from patent WO9741440.
ACCESSION   A66389
VERSION   A66389.1   GI:4538076
KEYWORDS
SOURCE   unidentified.
ORGANISM   unidentified
             unclassified.
REFERENCE   1 (bases 1 to 36)
AUTHORS   Burg,S.H., Kast,W.M., Toes,R.E., Offringa,R., Mellef,C. and
             Johannes,M.
TITLE   METHODS FOR SELECTING AND PRODUCING T CELL PEPTIDE EPITOPES AND
             VACCINES INCORPORATING SAID SELECTED EPITOPES
JOURNAL   Patent: WO 9741440-A 316 06-NOV-1997;
             UNIV LEIDEN (NL)
FEATURES
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             /db_xref="taxon:32644"

                                                                    29-MAR-1999

BASE COUNT   9 a   9 c   7 g   11 t
ORIGIN

Query Match   52.0%; Score 13; DB 6; Length 36;
Best Local Similarity 76.2%; Pred. No. 8.1e+04;

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Matches   16;   Conservative   0;   Mismatches   5;   Indels   0;   Gaps   0;

Qy      4 gctcgccccattaacatatt 24
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Db      1 GCTAGAGCCCATTACAAATATT 21
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RESULT 15
AF071603/c
LOCUS       AF071603        50 bp      DNA              ROD        26-JAN-1999
DEFINITION  Mus musculus clone CPJ-11 immunoglobulin heavy chain D-J region
            (VHJ558-D-J) gene, partial sequence.
ACCESSION   AF071603
VERSION     AF071603.1   GI:3290190
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Klonowski,K.D., Primiano,L.L. and Monestier,M.
  TITLE     Atypical VH-D-JH rearrangements in newborn autoimmune MRL mice
  JOURNAL   J. Immunol. 162 (3), 1566-1572 (1999)
  MEDLINE   99138837
REFERENCE   2  (bases 1 to 50)
  AUTHORS   Monestier,M. and Klonowski,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-1998) Microbiology and Immunology, Temple
            University School of Medicine, 3400 N. Broad St., Philadelphia, PA
            19140, USA
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="C3H +/+"
                     /db_xref="taxon:10090"
                     /tissue_type="liver"
                     /dev_stage="newborn"
     misc_feature    /rearranged
                     /clone="CPJ-11"
                     <1..>50
                     /gene="VHJ558-D-J"
                     /note="possible frameshift at D-J junction during
                     rearrangement may result in nonfunctional immunoglobulin
                     heavy chain"
     gene            <1..>50
                     /gene="VHJ558-D-J"
BASE COUNT     11 a     11 c     16 g     12 t
ORIGIN
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Query Match           52.0%;   Score 13;   DB 10;   Length 50;
Best Local Similarity 76.2%;   Pred. No. 8.1e+04;
Matches  16; Conservative  0; Mismatches  5; Indels  0; Gaps  0;

Qy      5 ctcgccccattaacatatc 25
          || | |||||| ||||| || ||
Db     33 CTTGGCCCCAGTAACGTAGTC 13
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Search completed: March 9, 2002, 00:48:39
Job time: 11120 sec